CURRENT STATUS OF OCCURRENCE, GENETIC DIVERSITY AND EPIDEMIOLOGY OF BANANA (*Musa* spp.) VIRUSES IN DEMOCRATIC REPUBLIC OF CONGO

L.F.T. Mukwa(1)(2), A.Gillis(3), V.Vanhese(1)., G., Romay(1)., S.Galzi(4)., N.Laboureau(4)., A.Kalonji-Mbuyi(2)(5), M-L. Iskra-Caruana(4), C.Bragard(1,2)*

(1) Université catholique de Louvain, Earth and Life Institute (ELI), Applied Microbiology – Phytopathology, Croix du Sud 2 Bte L07.05.03, 1348 Louvain-la-Neuve, Belgium;
(2) Clinique des Plantes de Kinshasa, D.R of Congo;
(3) Université catholique de Louvain, ELI, Applied Microbiology Laboratory of Food and Environmental Microbiology.
(4) CIRAD, UMR BGPI, F-34398, Montpellier Cedex 5, France;
(5) Université de Kinshasa.
(*) Corresponding author: claude.bragard@uclouvain.be

BACKGROUND and OBJECTIVES

Viruses are major constraints to the production and exchange of banana and plantain (*Musa* spp.) germplasm in the world. Several viruses are recognized to affect *Musa* spp: *Banana bunchy top virus* (BBTV*), Banana streak GF virus* (BSGFV), *Banana streak OL virus* (BSOLV*), Banana streak IM virus* (BSIMV)*, Banana streak MY virus* (BSMYV), *Cucumber mosaic virus* (CMV)*, Banana bract mosaic virus,* (BBrMV). To date, in Democratic Republic of Congo (DRC), except BBTV, others banana viruses are not yet reported. The main aim of this work was to elucidate the epidemiological situation, genetic variability and origin of *Musa* spp. viruses in DRC.

MATERIALS and METHODS

Epidemiological surveys were conducted from 2011-2013, in DRC, to search main viruses of *Musa* spp. Up to 666 samples collected from 122 locations; Samples were analysed using PCR based method. Detected viruses were sequenced and phylogenetic studies were performed.

RESULTS

BBTV is the most widespread virus (frequency=44,8%) in DRC. Molecular analyses support infrequent BBTV dispersal events between continents. This study reveals a low genetic variability of DRC BBTV isolates. They are close, gather in the South Pacific group and are linked with isolates of other sub-Saharan Africa (SSA) countries, but no with Egyptian isolates. Since the earliest BBTV report in SSA was in DRC in 1950, it is likely that BBTV spread from DRC to other SSA countries rather than from Egypt and that at least two BBTV introductions occurred in Africa. Haplotypes analysis based on the coding region m-Rep protein showed 38 haplotypes (haplotype diversity value of 0.944±0.013).
In Bas Congo, symptoms of Banana streak disease were associated to the presence of BSV species (frequency=19,9%); the most widespread were BSGFV (frequency=67,2%) and (BSOLV) (frequency=24,2%). The sequenced BSOLV isolate from *Musa acuminata*, gather in the clade I recognized to gathering the BSV species with endogenous counterpart. CMV was also detected (frequency=9,3%). Genetic diversity analysis reveals the high similarity between DRC CMV isolates with a South African isolate). BBrMV was not detected in collected samples.

CONCLUSION

DRC is a place of high prevalence of banana viruses, indicating the need for an improved quality of planting material. DRC seems to be the primary center of BBTV spread in Africa. BSV species data revealed the activation of endogenous BSV and the transmission of BSV species from plantain (B genome) to banana (A genome), in natural conditions. While for CMV, data suggest the hypothesis of a unique introduction through infected planting material and the distribution of a single strain of CMV. The BBrMV still absent in DRC.

Building bridges between disciplines for sustainable management of plant virus diseases

13th International Plant Virus Epidemiology Symposium

6-10 june 2016, Avignon, FRANCE

Programme and Abstracts